Section: Cell and Membrane Research

Orientational dynamics in lipid-protein model systems as observed by time-resolved fluorescence anisotropy

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Lipid-protein interaction in membranes is studied using liposomes of dimyristoylphosphatidylcholine and melittin as a model system. Melittin is a small polypeptide consisting of a sequence of six polar amino acids followed by a sequence of twenty hydrophobic amino acids, which incorporates into the lipid bilayer in a α-helical conformation. Time-resolved fluorescence anisotropy of diphenylhexatriene (DPH) as an indicator of lipid dynamics and of the tryptophan residue of melittin as an indicator of internal protein dynamics is measured yielding orientational relaxation times and orientational order parameters (1). Thus kinetic as well as structural information can be obtained for lipid and protein.

Incorporation of melittin into the ordered lipid phase does not affect the lipid relaxation time nor the lipid order parameter. In the fluid phase, however, melittin increases the lipid order, but again leaves the relaxation time unchanged. This indicates that melittin acts on the lipid order simply via steric hindrance.

The tryptophan relaxation time and order parameter are smaller than the correponding values for DPH. Thus as far as the motion of the amino acid side chain is concerned this is faster and less restricted than the motion of lipid chains.

1) Jähnig, F., (1979) Proc.Natl.Acad.Sci. USA 76, 6361.